

## WEST Search History





DATE: Wednesday, September 13, 2006

**Hide? Set Name Query****Hit Count***DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR*

<input type="checkbox"/>	L21	L9 and DNA adj adjuvant	6
<input type="checkbox"/>	L20	cytomegalovirus and CTL adj epitope and pan?HLA?DR and fus\$ not diamond.in.	1
<input type="checkbox"/>	L19	cytomegalovirus and CTL adj epitope and pan?HLA?DR not diamond.in.	1
<input type="checkbox"/>	L18	L9 and CTL adj epitope and pan?HLA?DR not diamond.in.	0
<input type="checkbox"/>	L17	L9 and CTL adj epitope and helper adj epitope not diamond.in.	1
<input type="checkbox"/>	L16	L10 and CTL adj epitope and helper adj epitope not diamond.in.	4
<input type="checkbox"/>	L15	L14 and "pp65"	9
<input type="checkbox"/>	L14	L13 and PADRE	11
<input type="checkbox"/>	L13	L12 and fusion	16
<input type="checkbox"/>	L12	L10 and CTL adj epitope and helper adj epitope	16
<input type="checkbox"/>	L11	L10 and L9	2
<input type="checkbox"/>	L10	helper same CTL near epitope same fusion	29
<input type="checkbox"/>	L9	cytomegalovirus near vaccine	66
<input type="checkbox"/>	L8	helper same CTL near epitope same fusion same PADRE	18
<input type="checkbox"/>	L7	helper same CTL near epitope same fusion same PADRE same "pp65"	2

END OF SEARCH HISTORY

(FILE 'HOME' ENTERED AT 14:28:51 ON 13 SEP 2006)

FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 14:29:29 ON  
13 SEP 2006

L1	0 "PP65" (S) PAN!HLA!DR
L2	45 CTL(S) HELPER(S) EPITOPE(S) FUS?
L3	1676 CYTOMEGALOVIRUS(S) VACCINE
L4	0 PAN!HLA!DR
L5	678 PADRE
L6	2 L2 AND L3
L7	2 L6 AND L5
L8	1 DUP REM L7 (1 DUPLICATE REMOVED)

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: September 3, 2005, 00:31:19 ; Search time 687.984 Seconds  
 (without alignments)  
 1338.184 Million cell updates/sec

Title: US-10-603-094-10  
 Perfect score: 19  
 Sequence: 1 gggggacgatcgtcggggg 19

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : GenEmbl:\*  
 1: gb\_ba:\*  
 2: gb\_htg:\*  
 3: gb\_in:\*  
 4: gb\_om:\*  
 5: gb\_ov:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pl:\*  
 9: gb\_pr:\*  
 10: gb\_ro:\*  
 11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	6	AX104767	AX104767 Sequence	
2	19	100.0	19	6	AX547820	AX547820 Sequence	
3	19	100.0	20	6	CQ753460	CQ753460 Sequence	
4	19	100.0	20	6	AX105109	AX105109 Sequence	
5	19	100.0	20	6	AX105234	AX105234 Sequence	
6	19	100.0	20	6	AX774077	AX774077 Sequence	
7	19	100.0	20	6	AX786663	AX786663 Sequence	
8	19	100.0	20	6	AX799756	AX799756 Sequence	
9	19	100.0	21	6	CQ753461	CQ753461 Sequence	
10	19	100.0	21	6	AX104805	AX104805 Sequence	
11	19	100.0	21	6	AX104806	AX104806 Sequence	
12	19	100.0	21	6	AX105117	AX105117 Sequence	
13	19	100.0	21	6	AX105118	AX105118 Sequence	

14	19	100.0	21	6	AX547858	AX547858	Sequence
15	19	100.0	21	6	AX547859	AX547859	Sequence
16	19	100.0	22	6	CQ753462	CQ753462	Sequence
17	19	100.0	24	6	CQ753463	CQ753463	Sequence
18	19	100.0	26	6	CQ753464	CQ753464	Sequence
19	19	100.0	28	6	CQ753465	CQ753465	Sequence
20	19	100.0	30	6	CQ753475	CQ753475	Sequence
21	19	100.0	30	6	CQ753476	CQ753476	Sequence
22	19	100.0	30	6	AX771754	AX771754	Sequence
23	19	100.0	30	6	AX771755	AX771755	Sequence
24	18	94.7	19	6	CQ753459	CQ753459	Sequence
25	18	94.7	20	6	AX104883	AX104883	Sequence
26	18	94.7	20	6	AX105137	AX105137	Sequence
27	18	94.7	20	6	AX547936	AX547936	Sequence
28	17.4	91.6	20	6	AX104803	AX104803	Sequence
29	17.4	91.6	20	6	AX104804	AX104804	Sequence
30	17.4	91.6	20	6	AX105115	AX105115	Sequence
31	17.4	91.6	20	6	AX105116	AX105116	Sequence
32	17.4	91.6	20	6	AX547856	AX547856	Sequence
33	17.4	91.6	20	6	AX547857	AX547857	Sequence
34	17	89.5	19	6	AX104879	AX104879	Sequence
35	17	89.5	19	6	AX105134	AX105134	Sequence
36	17	89.5	19	6	AX547932	AX547932	Sequence
37	16.4	86.3	1776	6	AR041208	AR041208	Sequence
38	16.4	86.3	1776	8	ASNRHGBA	L35500	Aspergillus
c 39	16.4	86.3	110000	1	AE016822_07	Continuation (8 of	
40	16.4	86.3	281450	1	AP005032	AP005032	Streptomy
41	16	84.2	4120	1	MFO238973	AJ238973	Mycobacte
42	16	84.2	11441	12	AY266291	AY266291	Escherich
43	16	84.2	195859	14	AF281817	AF281817	Tupaia he
44	15.8	83.2	20	6	AX104799	AX104799	Sequence
45	15.8	83.2	20	6	AX105114	AX105114	Sequence

## ALIGNMENTS

## RESULT 1

AX104767

LOCUS AX104767 19 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 959 from Patent WO0122972.

ACCESSION AX104767

VERSION AX104767.1 GI:13920964

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.

TITLE Immunostimulatory nucleic acids

JOURNAL Patent: WO 0122972-A 959 05-APR-2001;

UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)

FEATURES Location/Qualifiers

source

1..19

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

## ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACGATCGTCGGGGG 19

|||||

Db

1 GGGGGACGATCGTCGGGGG 19